



IFW16

RAW SEQUENCE LISTING

DATE: 08/18/2004

PATENT APPLICATION: US/09/492,971A

TIME: 09:27:18

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08182004\I492971A.raw

3 <110> APPLICANT: Vogel et al., Tikva
 5 <120> TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND USES AND METHODS OF
 PRODUCING SAME
 7 <130> FILE REFERENCE: 25775-CZ-AZ-A
 9 <140> CURRENT APPLICATION NUMBER: US 09/492,971A
 10 <141> CURRENT FILING DATE: 2000-01-27
 12 <160> NUMBER OF SEQ ID NOS: 38
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 11
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Synthetic Probe directed to Human Fibronectin
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 40 <210> SEQ ID NO: 3
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 42 <212> TYPE: DNA
 43 <213> ORGANISM: Artificial Sequence
 45 <220> FEATURE:
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 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 43
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Synthetic Probe directed to Human Fibronectin
 60 <400> SEQUENCE: 4
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 64 <210> SEQ ID NO: 5
 65 <211> LENGTH: 45
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial Sequence

ENTERED

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69 <220> FEATURE:
70 <223> OTHER INFORMATION: Synthetic Probe directed to Human Fibronectin
72 <400> SEQUENCE: 5
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76 <210> SEQ ID NO: 6
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79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
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84 <400> SEQUENCE: 6
85 acaatctacc atcatccagc cttggtaggg cttctccac gtttc          45
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174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
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186 <212> TYPE: PRT
187 <213> ORGANISM: Homo Sapiens
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192 1 5 10 15
195 Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln
196 20 25 30
199 Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys
200 35 40 45
203 Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu
204 50 55 60
207 Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val
208 65 70 75 80
211 Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr
212 85 90 95
215 Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg
216 100 105 110
219 Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg
220 115 120 125
223 Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn

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224	130					135					140					
227	Gly	Lys	Gly	Glu	Trp	Thr	Cys	Lys	Pro	Ile	Ala	Glu	Lys	Cys	Phe	Asp
228	145					150					155					160
231	His	Ala	Ala	Gly	Thr	Ser	Tyr	Val	Val	Gly	Glu	Thr	Trp	Glu	Lys	Pro
232						165					170					175
235	Tyr	Gln	Gly	Trp	Met	Met	Val	Asp	Cys	Thr	Cys	Leu	Gly	Glu	Gly	Ser
236						180					185					190
239	Gly	Arg	Ile	Thr	Cys	Thr	Ser	Arg	Asn	Arg	Cys	Asn	Asp	Gln	Asp	Thr
240						195					200					205
243	Arg	Thr	Ser	Tyr	Arg	Ile	Gly	Asp	Thr	Trp	Ser	Lys	Lys	Asp	Asn	Arg
244						210						215				220
247	Gly	Asn	Leu	Leu	Gln	Cys	Ile	Cys	Thr	Gly	Asn	Gly	Arg	Gly	Glu	Trp
248	225					230						235				240
251	Lys	Cys	Glu	Arg	His	Thr	Ser	Val	Gln	Thr	Thr	Ser	Ser	Gly	Ser	Gly
252						245					250					255
255	Pro	Phe	Thr	Asp	Val	Arg	Ala	Ala	Val	Tyr	Gln	Pro	Gln	Pro	His	Pro
256						260					265					270
259	Gln	Pro	Pro	Pro	Tyr	Gly	His	Cys	Val	Thr	Asp	Ser	Gly	Val	Val	Tyr
260						275					280					285
263	Ser	Val	Gly	Met	Gln	Trp	Leu	Lys	Thr	Gln	Gly	Asn	Lys	Gln	Met	Leu
264						290						295				300
267	Cys	Thr	Cys	Leu	Gly	Asn	Gly	Val	Ser	Cys	Gln	Glu	Thr	Ala	Val	Thr
268	305					310					315					320
271	Gln	Thr	Tyr	Gly	Gly	Asn	Leu	Asn	Gly	Glu	Pro	Cys	Val	Leu	Pro	Phe
272						325					330					335
275	Thr	Tyr	Asn	Gly	Arg	Thr	Phe	Tyr	Ser	Cys	Thr	Thr	Glu	Gly	Arg	Gln
276						340					345					350
279	Asp	Gly	His	Leu	Trp	Cys	Ser	Thr	Ser	Asn	Tyr	Glu	Gln	Asp	Gln	
280						355					360					365
283	Lys	Tyr	Ser	Phe	Cys	Thr	Asp	His	Thr	Val	Leu	Val	Gln	Thr	Gln	Gly
284						370					375					380
287	Gly	Asn	Ser	Asn	Gly	Ala	Leu	Cys	His	Phe	Pro	Phe	Leu	Tyr	Asn	Asn
288	385					390					395					400
291	His	Asn	Tyr	Thr	Asp	Cys	Thr	Ser	Glu	Gly	Arg	Arg	Asp	Asn	Met	Lys
292						405					410					415
295	Trp	Cys	Gly	Thr	Thr	Gln	Asn	Tyr	Asp	Ala	Asp	Gln	Lys	Phe	Gly	Phe
296						420					425					430
299	Cys	Pro	Met	Ala	Ala	His	Glu	Glu	Ile	Cys	Thr	Thr	Asn	Glu	Gly	Val
300						435					440					445
303	Met	Tyr	Arg	Ile	Gly	Asp	Gln	Trp	Asp	Lys	Gln	His	Asp	Met	Gly	His
304						450					455					460
307	Met	Met	Arg	Cys	Thr	Cys	Val	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Thr	Cys
308	465					470					475					480
311	Ile	Ala	Tyr	Ser	Gln	Leu	Arg	Asp	Gln	Cys	Ile	Val	Asp	Asp	Ile	Thr
312						485					490					495
315	Tyr	Asn	Val	Asn	Asp	Thr	Phe	His	Lys	Arg	His	Glu	Glu	Gly	His	Met
316						500					505					510
319	Leu	Asn	Cys	Thr	Cys	Phe	Gly	Gln	Gly	Arg	Gly	Arg	Trp	Lys	Cys	Asp
320						515					520					525

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323 Pro Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile
324      530                      535                      540
327 Gly Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr
328 545                      550                      555                      560
331 Cys Tyr Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr
332                      565                      570                      575
335 Tyr Pro Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro
336                      580                      585                      590
339 Ser Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser
340      595                      600                      605
343 His Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly
344      610                      615                      620
347 Arg Trp Lys Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile
348 625                      630                      635                      640
351 Lys Gly Leu Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile
352                      645                      650                      655
355 Gln Gln Tyr Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr
356                      660                      665                      670
359 Ser Thr Ser Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr
360      675                      680                      685
363 Pro Phe Ser Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr
364      690                      695                      700
367 Ala Ser Ser Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser
368 705                      710                      715                      720
371 Gly Phe Arg Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln
372      725                      730                      735
375 Tyr Leu Asp Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu
376      740                      745                      750
379 Leu Pro Gly Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp
380      755                      760                      765
383 Gly Glu Gln Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp
384      770                      775                      780
387 Ala Pro Pro Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val
388 785                      790                      795                      800
391 Val Arg Trp Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val
392      805                      810                      815
395 Tyr Ser Pro Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu
396      820                      825                      830
399 Thr Ala Asn Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr
400      835                      840                      845
403 Asn Ile Thr Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val
404      850                      855                      860
407 Val Ile Gln Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro
408 865                      870                      875                      880
411 Ser Pro Arg Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr
412      885                      890                      895
415 Ile Met Trp Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp
416      900                      905                      910
419 Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/18/2004
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

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